DOCKET NO.: IBIS0007 **PATENT**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Ecker, Griffey, Crooke, Sampath, Swayze, Mohan, Hofstadler, and McNeil

Serial No.: **09/076,404** Group Art Unit: **1631**

Filed: **May 12, 1998** Examiner: **A. Marschel**

For: **MODULATION OF MOLECULAR INTERACTION SITES ON RNA AND OTHER BIOMOLECULES**

Assistant Commissioner
for Patents,
Washington, D.C. 20231

Dear Sir:

Declaration of Dr. David J. Ecker Under 37 C.F.R. §1.132

I, David J. Ecker, hereby declare as follows:

1. I am Vice President & Managing Director of Ibis Therapeutics, a division of Isis Pharmaceuticals, the assignee of the above-identified application.

2. I am a co-inventor of subject matter claimed in the above-identified application.

3. Page 94, lines 29-31 of the above-identified patent application as filed recites "Software packages from companies such as, for example, Tripos (St. Louis, MO), Molecular Simulations (San Diego, CA), MDL Information Systems (San Leandro, CA) and Chemical Design (NJ) provide means for computational generation of structures."

4. One skilled in the art, having examined Applicants' entire specification, would have recognized that the software package referred to in the specification and available from Tripos is called "Sybil/Base," that the software package referred to in the specification and available from Molecular Simulations is called "Insight II," and the software package referred to in the specification and available from MDL Information Systems is called "Sculpt."

5. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the applications or any patent issued thereon.

Date: 6-13-01

David J. Ecker

Dr. David J. Ecker

BASE

A Single Gateway to Molecular Design and Analysis

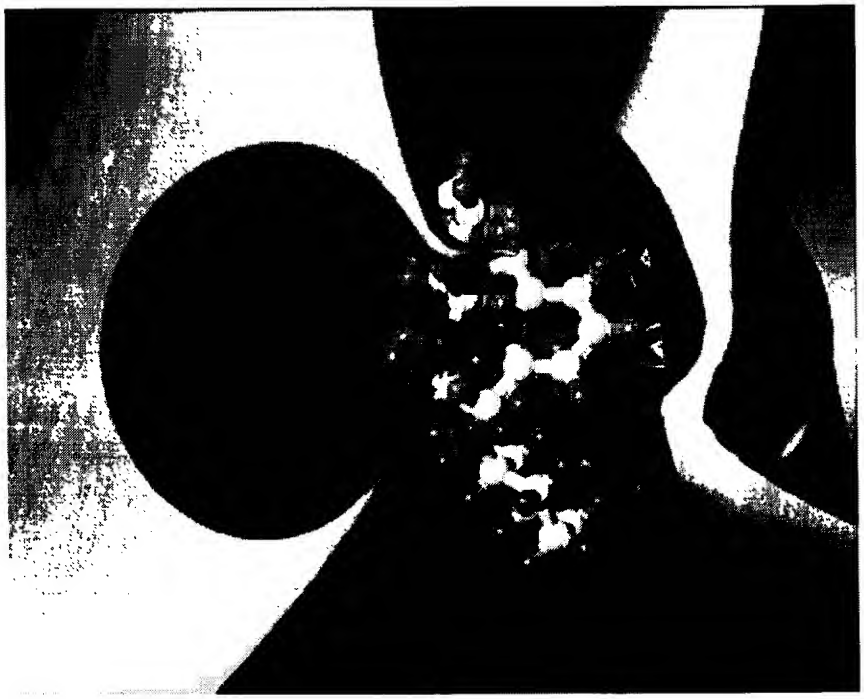
SYBYL®/Base, the heart of Tripos Discovery Software, provides the fundamental components for understanding molecular structure and properties with a special focus on the creation of new chemical entities. SYBYL/Base provides essential construction, editing, and visualization tools for both large and small molecules.

Data organization and analysis rely on the Molecular Spreadsheet™, which integrates chemical information with standard data manipulation tools. SYBYL's programming language and open architecture facilitate customized drug design methods.

Applications

- ✦ Visualize and investigate new chemical entities
- ✦ Organize and share molecular data via the Molecular Spreadsheet™
- ✦ Construct and refine molecular models
- ✦ Unify data from diverse sources
- ✦ Create custom drug discovery methods

An enzyme mimic this small organomanganese complex duplicates the catalytic activity of superoxide dismutase a 31KD protein. The complex is rendered in ball-and-stick mode and shown with an isopotential contour.

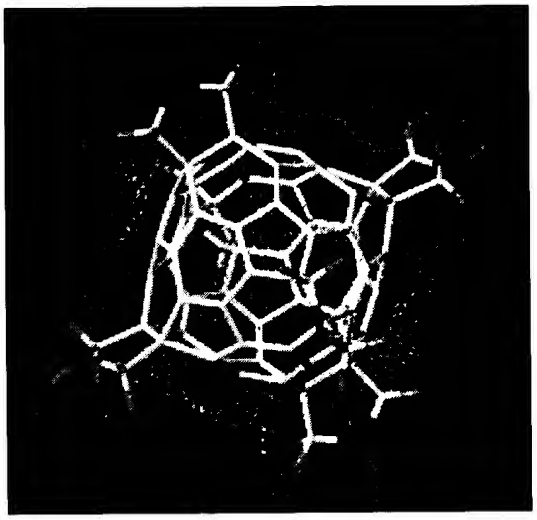


Building and Editing

Features

- 3D sketching
- Libraries of common molecules and functional groups
- Interface to the Cambridge Structural Database
- Editing of existing atoms, bonds, geometry, stereochemistry, and conformation
- Support for many file formats

Sketch... Import/Export... Revise



An electroluminescent fullerene rendered as capped sticks and surrounded by a dot surface color-coded by atomic charge.

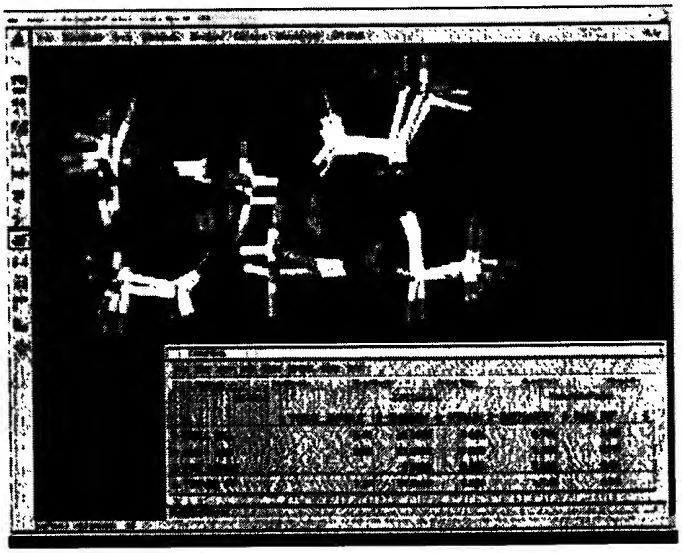
Molecular structures can be entered from a variety of sources. SYBYL/Base reads many formats, including MDLi MOL and SD, Cambridge Structural Database, Protein Data Bank, and SMILES. Direct entry of structures is also possible using SYBYL's sketcher or 3D building tools. Editing of existing structures requires only a simple point-and-click to alter atoms, bonds, isomerization, or stereochemistry. Bond distances, bond angles, and torsions may also be modified. Large and small molecules are modeled in the same window, with no requirement for an elaborate setup process.

Computation

Features

- Tripos, Amber, MM2 and MMFF94 force fields
- Periodic boundary conditions for energy calculations and minimization
- Constrained minimization
- Multiple charge calculation methods
- Solvent models including the Molecular Silverware™ solvent packing algorithm
- Molecular superpositioning
- Field fitting
- Manual interactive docking
- MOPAC 6
- Interfaces to Gaussian, MOPAC, EHMO and Connolly

Molecular & Quantum Mechanics... Manual Docking... Superpositioning



A cyclic hexapeptide optimized using several different force fields. The results are compared by superimposing the optimized structures and by measuring geometric and energetic properties within the Molecular Spreadsheet.

Geometry optimization (minimization) is performed via molecular mechanics or quantum mechanical methods to produce high quality models. SYBYL/Base offers a variety of force fields as well as several options for computing or importing atomic charges. Several algorithms are available for generating solvent models.[1] Geometric features such as planes, normals, and centroids can be defined. Distance, angle, and torsion constraints for minimization can be keyed to individual atoms or geometric features. Computational resources and local geometries can be conserved by defining aggregates of rigid atoms. Field fit options drive two or more structures in the direction of shape and electrostatic similarity. Multiple structures can also be compared using several different approaches to molecular superpositioning.

Analysis and Organization

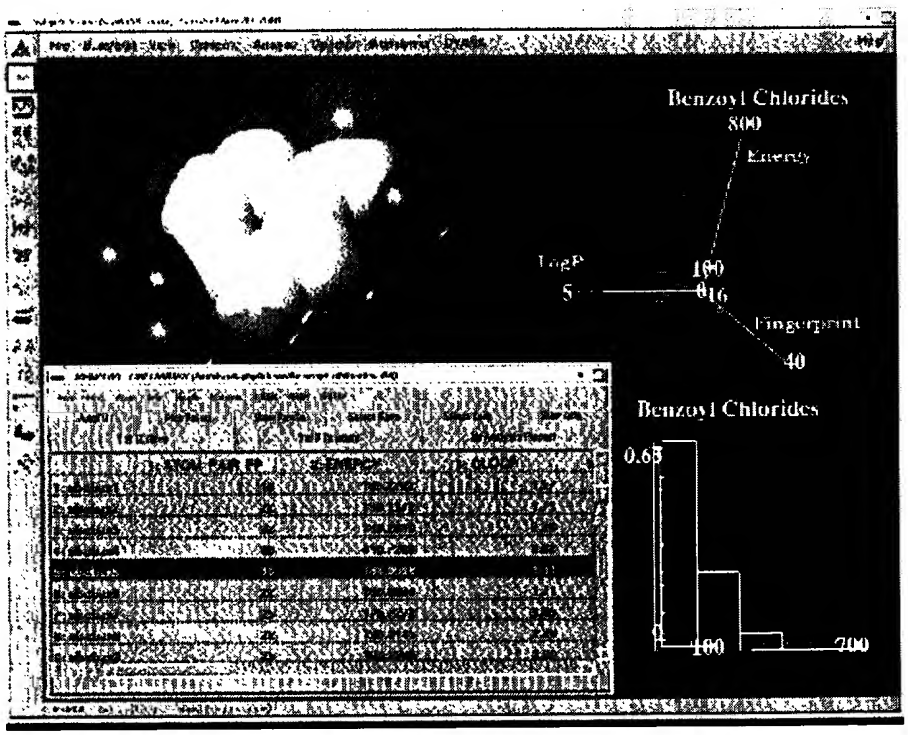
Features

- Analyze sets of molecules
- Measure distances, angles, and torsions
- Interactive monitoring of distances and hydrogen bonds
- Basic spreadsheet functionality
- Dynamic connection among MSS, displayed molecules, and graphs
- Unlimited number of rows and columns
- Over 60 built-in metrics, including MW, distances, angles, and torsions
- Scatter plots, histograms, isocontour, and mesh plots
- Automatic 2D depictions of molecules
- Print results to files, printers or an HTML table
- Easily define new column types

Molecular Spreadsheet... Geometric Measurements... Interactive Graphs

SYBYL/Base contains built-in tools for analysis of molecular structure, as well as the interactive Molecular Spreadsheet. Geometric features such as distances, angles, and torsions can be measured statically or monitored interactively. Topographical data and other molecular information can be listed and exported. SYBYL/Base calculates single point energies from a variety of force fields.

The Molecular Spreadsheet (MSS) organizes the analysis of molecule sets. Rows represent molecules, and columns contain related metrics such as molecular weight, topographical data, energies, and biological activity. Over 60 built-in metrics are available in SYBYL/Base, with others provided by additional modules. The MSS supports unlimited numbers of rows and columns, as well as standard spreadsheet functionalities including sorting, filtering, and basic statistics.



The Molecular Spreadsheet provides data organization, automatic metric generation, and visualization capabilities. Interactivity between graphs, the spreadsheet, and molecular displays speed the identification of relationships within data. When a graph point is selected, the related row is highlighted and the corresponding structure is displayed.

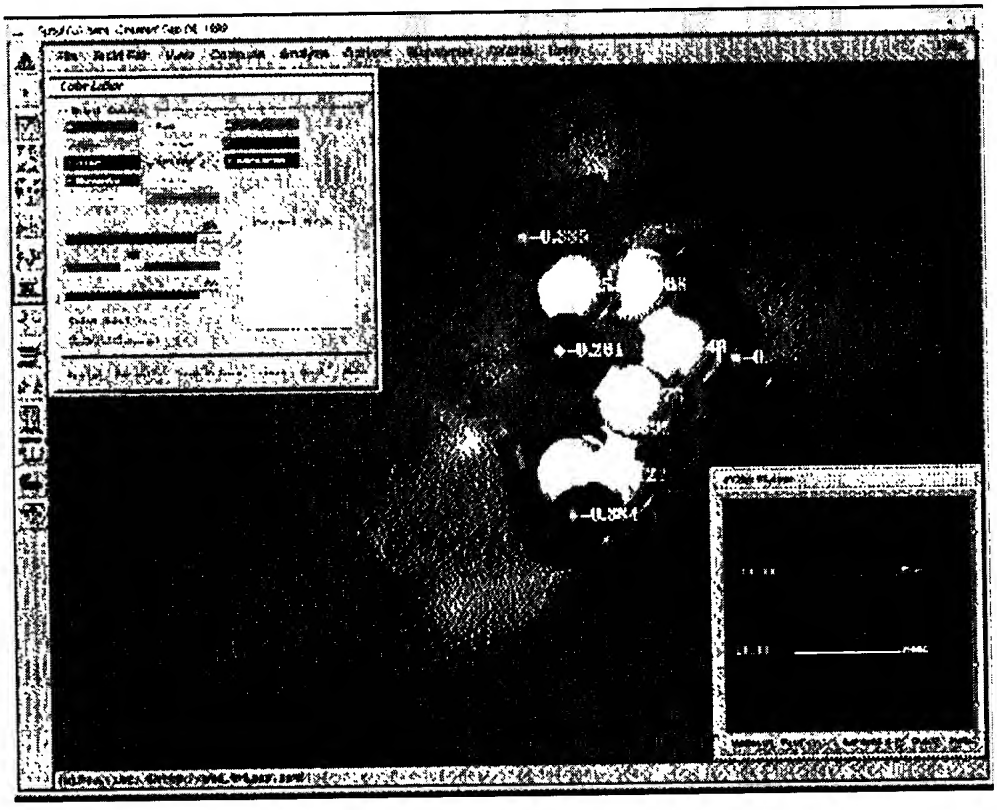
Scatter plots, histograms, isocontours, and mesh plots provide additional ways to investigate data. The molecules from MSS rows can be viewed in 3D or automatically depicted as 2D images. The MSS, data graphs, and molecular displays are dynamically connected — clicking on a cell instantly highlights related graph points and displays the associated molecule. New column types are built from equations, combinations of other columns, or entirely new routines written in the SYBYL Programming Language. Information in the MSS can be exported in several ASCII file formats, as an HTML table, or printed.

Visualization

Features

- Line, stick, ball-and-stick, or spacefilling representations, alone or in combination
- Dots, grids, contours, and opaque surfaces
- Full control of colors, labels, and screen annotation
- High quality output to PostScript, GIF, and TIFF formats
- Toolbar to manipulate visual options

SYBYL/Base offers extensive display options. Molecules can be displayed as lines, sticks, ball-and-stick, or spacefilling spheres. These representations can be mixed for additional emphasis or to highlight key portions of a molecule. Colors, labels, depth cueing, shading, stereo view mode, and Z-clipping can be readily changed through the SYBYL toolbar. Volume displays, contours, grids, and dotted surfaces provide the ability to visualize molecular properties. Images on the screen can be scaled, rotated, and translated using the mouse, the virtual dialbox, or the keyboard. Views can be annotated with arrows and text, either in 2D or with elements that rotate and translate with the molecules. These views can be captured at printer or screen resolution in PostScript™, GIF, or TIFF formats for inclusion in electronic documents or for hard copy.



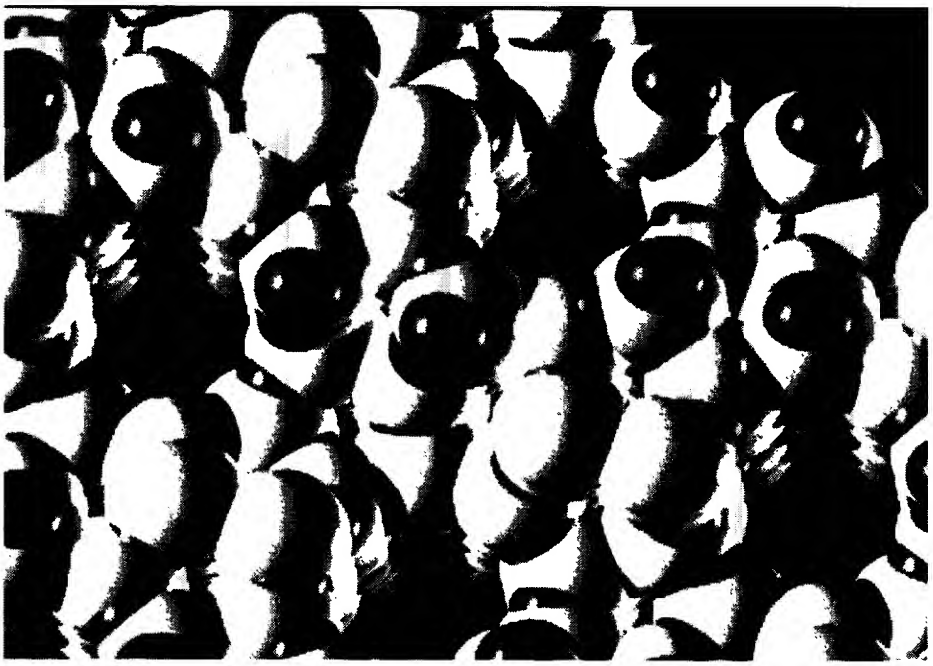
SYBYL/Base allows complete control of graphic displays, including colors, labels, annotations, depth cueing and z-clipping. Vitamin C is shown below in ball-and-stick mode with a recolored and z-clipped isopotential surface. Point charges are labeled. The toolbar at the far left provides access to tools such as the color editor, which makes it possible to prepare a custom color palette for objects and backdrops.

Customization

Features

- Create completely new computational methods
- Customize the SYBYL interface
- Directly access hundreds of callable SYBYL commands and functions
- SPL control of graphics and display
- Automate repetitive tasks

SYBYL/Base enables custom drug design methods via the SYBYL Programming Language (SPL). SPL connects, automates, and integrates existing functionality while providing the ability to create new user interfaces and entirely new computational techniques. Expression generators within SPL return information about atoms, bonds, substructures, molecules, tables, and graphics. SPL programs can combine this information with SYBYL commands to create specific research methodologies. SPL accesses UNIX shell scripts so that external software programs can be run and their results combined with SYBYL computations.



A zeolite rendered as CPK spheres. The knowledge of crystallographic space groups within SYBYL/Base simplifies construction of complex molecules.

Groups of objects such as atoms, bonds, and substructures can be defined as named sets. These sets can be saved, used by SPL routines, or selected interactively. Parameters underlying the SYBYL commands can be modified. Energy terms are scalable and the parameters that comprise force field equations are customizable. These personal preferences can be included in a startup file. Journaling saves both commands and textual information returned by SYBYL for review or playback.

Validation

The force fields in SYBYL/Base have been extensively tested and validated against the literature. The validation of the Tripos force field[2] was based upon crystal structures of small molecules and peptides. SYBYL/Base includes implementations of the Amber united-atom and all-atom force fields,[3-6] as well as MMFF94[7-9] and MM2.[10]

Complementary Software

SYBYL/Base is the foundation for the Tripos total drug discovery system. The capabilities of SYBYL/Base can be expanded by licensing additional functionality to meet specialized research needs.

Molecular modeling and visualization

MOLCAD	MM3
AMPAC	Advanced Computation

Chemical information systems

UNITY	CONCORD
StereoPlex	

Combinatorial chemistry and molecular diversity

Selector	DiverseSoltuions
Legion/CombiLibMaker	

Pharmacophore perception

DISCO	RECEPTOR
FlexS	GASP

Structure-activty relationships

Charisma	QSAR with CoMFA
HQSAR	Advanced CoMFA

Macromolecule-based drug design

Biopolymer	SiteID
FlexX	CScore
LeapFrog	

Structural biology and bioinformatics

Composer	ProTable
GeneFold	MatchMaker

NMR analysis and structure generation

TRIAD	DYANA
CAPRI	MARDIGRAS+

Hardware and Software Requirements

SYBYL/Base requires a license and will run on SGI R4000 and higher platforms operating under IRIX 6.5 and higher.

References

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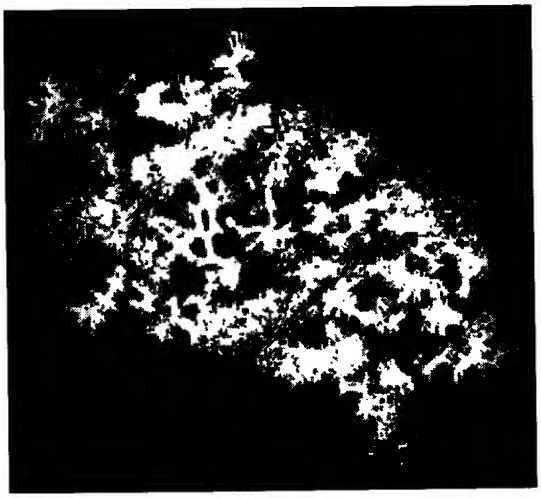
Insight II

An Integrated Modeling Environment

The major challenge today in the creation of biopharmaceutical products is to shorten the research and development cycle.

Efficiency of this product discovery process can be significantly improved by computer aided molecular design (CAMD).



NMR Refine Advanced provides a variety of advanced protocols for generating structures from NMR experimental data

CAMD enables you to simulate the structure, behavior, and interactions of molecules on computers. You can visualize dynamic changes in structures and predict how chemicals will interact over time. Through this graphical simulation, you can try a vast array of ideas and quickly focus on your most promising research projects.

Strategies to Advance Your Research

MSI's comprehensive suite of molecular modeling and simulation programs is changing the way you view chemistry. With MSI software, the rational design of structures using computer simulation to suggest compounds worthy of actual synthesis is possible. Structure determination of compounds through X-ray, NMR and homology techniques is available at your fingertips.

The Insight II® Environment

Insight II is a 3D graphics program which integrates an extensive suite of modeling tools. Its powerful, simple-to-use interface gives you a seamless flow of data between other MSI programs. The Insight II program is used to create, modify, manipulate, display, and analyze molecular systems and related data.

Other CAMD tools include Discover, a program for molecular mechanics and dynamics calculation, DeCipher, a highly flexible molecular structure and dynamics analysis program, CHARMm, a highly regarded and widely used simulation package, DelPhi for calculating electrostatic potential, MODELER for automatic homology model building, X-PLOR for macromolecular structure determination, and Ludi for de novo ligand design. You can apply these programs to a variety of applications in life science research.

Insight II's integrated approach facilitates rapid verification of simulated data against experimental data. Interactive data manipulation through tables and graphs helps you make decisions for fast, efficient work. You can access MSI's broad range of programs, as well as QCPE and other third-party programs and databases.

The novice user can make use of simple pull-down menus, while the advanced user has the option of accessing all of the commands through keyboard entry. Extensive context-sensitive on-line help capabilities, online documentation and tutorials, and reversible left- and right-hand menu orientations give you an easy to use, flexible working environment. In addition, you can store frequently-used command sequences for quick recall, and at any point, you can save a session and restore it later at the same point.

Techniques Integral to Insight II

Building

Insight II's set of modeling tools help you build molecular structures that can then be simulated and analyzed. Structures are constructed by sketching, aggregating fragments, applying symmetry operators, and importing from other systems.

Visualizing

Discovery of characteristics is greatly enhanced by visualizing structures and data. Insight II's advanced tools offer you a wide range of visualization options to suit your problem.

Analyzing

Analysis capabilities make it possible for you to draw meaningful conclusions from large amounts of otherwise difficult to interpret data.

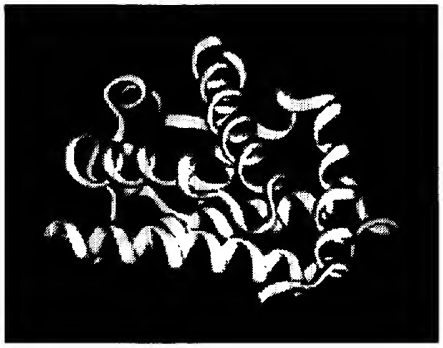
Automation and Customization Capabilities

You can customize Insight II to fit your specific needs or automate commonly performed tasks through the BCL Command Language and support is built in for many common file formats.

msi
molecular simulations

Insight II

An Integrated Modeling Environment



This image shows the result of a "Profiles 3D Verify" showing a ribbon drawing of a model of myoglobin, where a single alpha-helix has been purposely misfolded. Profiles-3D has detected the misfolded region, and Insight II has automatically created the subset that was used to color the structure and ribbon.

BCL Command Language

The BCL Command Language (BCL) is an Insight II feature for defining and executing macros. A macro can contain Insight II commands, variables, arithmetic expressions, conditionals, and loops. Once defined, the macro becomes a custom command.

The macro command is parsed and executed exactly like a standard Insight II command. You can also add the macro to the menu structure. A parameter block is automatically generated so you can enter the parameter values through the menu system. The advantage of macros is that they allow you to customize Insight II without changing the executable image.

Multiple File Formats

Insight II supports many different data file formats, including: Brookhaven and Cambridge databases; AMPAC/MOPAC, and QCPE programs; Molecular Design Limited Molfile and SD files; Sybyl MOL2 files; color PostScript HPGL compatible devices or VRML; and PICT files for Macintosh and IBM PC applications. Screen images can be output directly onto slide, polaroid, or print film with the Focus Graphics Imagemaker slide recorder, or onto paper media using HPGL plotters and PostScript printers.

Insight II Features

Visualizer

Visualizer gives you control of display styles, and the manipulation of molecules.

- View molecules in many ways by varying color and representation techniques (stick, CPK's, ribbons, etc.).
- Define colors of individual atoms or atom types, selected residues or residue types, and surface properties.
- Label atoms and residues by a variety of methods including chirality and prochirality.
- Generate non-molecular annotations, such as arrows and fonted text.
- Define molecular data files via a free format interface.
- Easily manipulate large and small molecules, including proteins, nucleic acids, carbohydrates, and polymer systems.
- Control real time translation, rotation, scaling, and Z plane clipping by dial or mouse.
- Superimpose molecules by least squares.
- Measure non-bond energies at the atom, residue, and molecule levels.
- Display tabular lists of atoms, residues, dihedral angles, distances, and hydrogen bonds.
- Display van der Waals or solvent accessible surfaces.
- Dynamically monitor inter/intra-atomic distances, and dihedral angles during torsional updating or relative positioning.
- Calculate and display hydrogen bonds.
- Display Richardson diagrams for protein structure visualization.

Builder

Builder easily builds and modifies molecules in 3D.

- Build 3D molecular systems from functional groups, templates, or monomeric units and residues.
- Modify such properties as atom type, hybridization, potential function parameters, bond order, and geometry.
- Automatically add hydrogens and soak molecules in waters or other solvents.
- Prepare molecules for subsequent mechanics simulations with the ability to select from Amber, CVFF, and CFF forcefields.

Analysis

Analysis analyzes structural features of molecules and atomic properties. The results can be displayed in graphs or as output to files.

- Accept, display, and animate output from Discover simulation trajectories or other programs.
- Monitor, correlate, and cross correlate interdependent properties, such as energies, distances, and angles.
- Create RMS cluster plots and perform analyses of conformational families.
- Create, query, and annotate 2D and 3D histograms and line graphs with data from external programs.
- Perform Fourier fitting to eliminate specified vibrational frequencies from simulation data.
- Analyze 3D grid data, such as electron density and electrostatic potential with wire frame and solid contours, and up to three independently-positionable slicing planes.

Spreadsheet

With the Insight II spreadsheet, you can create your own analyses.

- View textual and numerical data in a tabular format.
- Calculate data based on formulas, molecular properties, mathematical expressions, or other data in the spreadsheet.
- Use Insight II-generated spreadsheets to display properties of the structure you are studying.

- Perform searches to find structures of interest.
- See your spreadsheet data dynamically update as you change the geometry of the molecular structure.

Docking

Docking allows independent manipulation of molecules with interactive non-bond energy calculations.

- Manipulate molecules and collections of molecules, to perform docking exploration with bump checking.
- Calculate the interaction between two molecules using explicit van der Waals energy and/or Coulombic energy.
- Use an energy grid to quickly calculate the interaction energy between two molecules.

Hardware Requirements

Insight II versions available for Silicon Graphics and IBM RISC System/6000 workstations.

Software Tools

Modules in the Insight II environment provide solutions for X-ray and NMR structure determination, protein modeling, dynamics simulation and analysis, docking and structure-based drug design.

Affinity provides automated docking of ligands to receptors in the structure-based drug design process. These calculations include an implicit solvation term. The component effects of this solvation term and of other energetic partitions can be viewed graphically.

Biopolymer constructs models of peptides, proteins, carbohydrates, and nucleic acids for visualizing complex macromolecular structures.

CFF, an advanced Class II Force field, is used to optimize DNA, RNA, carbohydrates, lipids, proteins, peptides, and small-molecule models, giving a high confidence level for calculations in drug discovery, protein design, genomic therapeutics, NMR spectroscopy, and X-ray crystallography.

CHARMm combines standard minimization and dynamics capabilities with expert features including free energy perturbation (FEP), correlation analysis and combined quantum and molecular mechanics (QM/MM) methods.

Consensus builds a 3D model of a protein from its amino acid sequence and the known structures of related proteins using distance constraints derived from the reference protein structures.

Converter converts 2D structural databases into 3D structural databases.

DeCipher is a powerful and flexible program for high-level analysis of molecular structure and the results of molecular dynamics simulations.

DelPhi calculates electrostatic potentials and solvation energies of both large and small molecules, including nucleic acids. You can use DelPhi to rigorously examine the effects of charge distribution, ionic strength, and dielectric constant on the electrostatic potentials of macromolecules.

Discover incorporates a range of well validated forcefields for dynamics simulations, minimization, and conformational searches, allowing you to predict the structure, energetics and properties of organic, inorganic, organometallic, and biological systems.

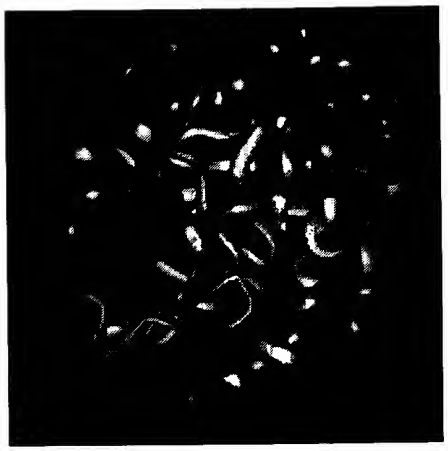
DMol is a quantum mechanics module which makes possible, fast, reliable, quantitative predictions of molecular structure, energetics and properties for ground and transition states. DMol employs advanced density functional theory (DFT).

Homology builds a 3D model of a protein from its amino acid sequence and the known structure of related proteins. Standard techniques of backbone building, loop modeling, structural overlay and statistical analysis of the resulting models are available.

Ludi is a powerful tool for de novo rational drug design. Ludi can be used to fit molecules into the active site of a receptor by identifying and matching complementary polar and hydrophobic groups.

Ludi/ACD links the design tools of Ludi to MDL's Available Chemicals Directory. Ludi/ACD provides access to over 65,000 commercially available structures to accelerate your search for drug candidates.

MADSYS is a program that provides phasing of multi-wavelength anomalous dispersion (MAD) data collected at synchrotron radiation X-ray sources.



MODELER, a module of Insight II, can create homology models in an automated fashion. The resulting models can be visualized and analyzed via Insight II's graphical interface.

Insight II

An Integrated Modeling Environment

MBO(N)D is a multibody dynamics program which allows you to produce simulations of molecular movements and properties up to 30 times faster than conventional methods.

MODELER automatically generates a refined homology model of a protein, given only the sequence alignment to a known 3D protein structure. You are able to generate excellent structural models given as little as 30% homology to known structures.

NMR Refine DGII provides an entry-level option into NMR refinement software with capabilities for generating structures from NMR-derived distance and dihedral restraints. The DG II, Restraint Analysis, NMR Database and ProStat pulldowns combine to give the NMR spectroscopist the necessary tools for generating, analyzing and verifying high resolution structures.

NMR Refine Advanced expands the refinement capabilities found in NMR Refine DG II to include simulated annealing and restrained molecular mechanics and dynamics (MD Schedule), refinement of NOE intensities using hybrid-matrix approaches (IRMA), direct refinement of NOE volumes (NOE-MD), an interface to back-calculating 2D NOESY crosspeak intensities (NOE Simulate), and a spreadsheet method of analyzing NMR-related structural and dynamical molecular parameters (Query).

NMR X-PLOR streamlines the steps in structure determination from NMR data. You can visualize your NMR restraints, directly set up and launch X-PLOR refinement calculations and evaluate the quality of the calculated structures.

Profiles-3D searches a structural-motif database with a new sequence, looking for compatibility; searches a sequence database with an example structure, seeking similarity; or verifies the agreement between the sequence and current model of a protein sequence/structure under study.

QuanteMM combines quantum mechanical and force field methods, allowing you to use accurate first-principles methods to study cluster models while taking the surrounding environment fully into account. Enables highly accurate simulations of active sites and systems such as metallo-proteins.

Search/Compare generates and compares the conformers of different molecules. You can operate on molecular fields and volumes, superimpose two or more molecules, and search systematically for sterically allowed conformations.

Sketcher is used to draw molecules in 2D and automatically convert them to 3D models.

Turbomole applies Hartree-Fock and density functional methods to predict molecular structure and energetics and numerous properties such as electrostatic potentials, molecular moments, and polarizabilities.

X-PLOR/DG is a macromolecular structure determination program that integrates NMR experimental data with molecular mechanics, dynamics and energy minimization to aid in the solution of three dimensional structures. This includes distance geometry, simulated annealing, restrained molecular dynamics, and relaxation matrix analysis.

X-PLOR/Refine is an X-ray structure determination program that integrates crystallographic diffraction data with molecular mechanics, dynamics and energy minimization to aid in the solution of three-dimensional structures.

Xsight integrates all of the major computational techniques for macromolecular crystallography. You can analyze and interpret X-ray data, build models of protein structures and relate them to electron density, refine structures against X-ray data, analyze structures for symmetry, and visualize and validate structures.

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SCULPT

Free 60-day SCULPT trial for Beilstein Commander 2000 users

Beilstein Commander 2000 now enables you to transfer structures to SCULPT for 3D viewing and analysis. Beilstein Commander 2000 and CrossFire 2000 are an integrated client/server application for searching the world's largest electronic collections of organic chemistry and inorganic and organometallic data: CrossFire Beilstein and CrossFire Gmelin.

New! SCULPT 3.0 Special Report

SCULPT is a desktop 3D visualization system built for chemists and biochemists. Its intuitive interface lets scientists quickly import compounds from ISIS to help understand steric, electrostatic, and conformational effects of ligands and ligand-receptor complexes. SCULPT 3.0 contains significant enhancements, including automatic alignment of compounds, electronic communication through OLE embedding, high-quality visualizations, and tighter integration with MDL products. See SCULPT's key features by viewing AVI movies or browsing through the SCULPT tutorials.

Buy SCULPT

Highlights:

Obtain 3D structural information: SCULPT automatically generates a low-energy 3D conformation when a scientist pastes a compound from ISIS/Draw, ISIS/Base, ISIS for Microsoft Excel, or Chime into SCULPT. Scientists can quickly determine the orientation and distance between functional groups, the size and volume of a compound, or important Rgroup, and the position and potential influence of hydrogen bond

MDL File Formats

donors and acceptors.

Explore and sample conformations: Three-dimensional conformation provides valuable information about steric and electrostatic attributes needed in binding. The interface to the conformational flexibility feature has the same intuitive feel of plastic and brass models. As the conformation changes, SCULPT interactively maintains valid bond geometry and non-bonded interactions.

Align compounds: SCULPT helps chemists discover structural relationships by automatically aligning compounds to each other or to a bound ligand using either its Maximal Common SubStructure (MCSS) or a Steric and Electrostatic properties (SEAL) algorithm.

Visualize 3D relationships: SCULPT provides high-quality visualizations including solvent-accessible surfaces, protein ribbons, contact surfaces, and CPK and ball-and-stick rendering.

Facilitate communication: SCULPT improves communication of 3D information among multidisciplinary groups. SCULPT objects can be stored in Microsoft Word or email documents to provide both images and live 3D objects that a reviewer can rotate and manipulate

SCULPT 3.0 enhancements:

- 3D alignment of compounds is automatic.
- A tree view allows easy operation and alignment of different molecules.
- Solvent-accessible surfaces show the shape of a receptor or aligned active molecules.
- New OpenGL graphics provide publication quality images and new visualization features.
- 2D-to-3D conversion is improved and can be applied to a list of molecules from an SDfile.
- Preservation of attributes in saved files enables easy communication of results to project members.
- Sets allow control over groups of molecules.
- OLE embedding improves communication of results.

Download Y2K tested SCULPT on SGI and Mac

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